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Genetic Polymorphism of Edilbay Sheep based on DNA Microsatellites

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The Edilbay sheep breed holds significant importance for the sheep industry in Kazakhstan due to its adaptability and high meat productivity. However, genetic information related to productivity traits in this breed remains limited. This study aimed to assess the genetic polymorphism of Edilbay sheep bred in West Kazakhstan using microsatellite DNA markers to identify loci potentially associated with productivity. A total of 75 sheep were divided into two groups based on productivity. Genomic DNA was extracted from hair follicles and analyzed using multiplex PCR. Genotyping was performed at 12 microsatellite loci, and results were evaluated using statistical and genetic diversity indices. The most polymorphic locus was INRA063 (15 alleles), while the least polymorphic was ETH152 (5 alleles). Highly productive sheep exhibited greater allelic diversity and higher levels of heterozygosity at certain loci (e.g., INRA006, MAF214, INRA023), suggesting possible associations with productivity. The identified polymorphic loci and their allele distributions provide a genetic basis for future marker-assisted selection (MAS) in Edilbay sheep breeding, contributing to more efficient resource use and improved meat production in harsh environments.

Keywords: Animal production, genetic diversity, indigenous breeds, marker assisted selection, eukaryotic genome, polymorphism.

INTRODUCTION

The assessment and preservation of livestock genetic diversity are essential components of sustainable animal production systems, particularly under the increasing pressures of climate variability and growing global demand for animal-based food products. Genetic characterization of local and indigenous breeds plays a critical role in identifying alleles associated with adaptive traits such as thermal tolerance, disease resistance, and feed efficiency – traits that are increasingly valuable in marginal environments. Despite this, many regionally adapted breeds remain poorly studied at the molecular level and are underrepresented in international genomic databases. The development and application of molecular markers, such as microsatellites, provide an effective means to assess intra- and inter-population variability and support the implementation of marker-assisted selection strategies. The choice of the West Kazakhstan region is since fat-tailed sheep breeding is one of the main fields in Kazakhstan's animal husbandry (Davletova et al., 2020). Fat-tailed sheep are characterized by high meat productivity and adaptability to unstable natural conditions, where other branches of agriculture are often practically impossible. Among the fat-tailed coarse-haired sheep of the meat-lard type, the Edilbay breed is of leading importance. It can compete with the outstanding early-maturing English factory sheep of meat-wool breeds in terms of high maturing rate and meat productivity (Kamalieva et al., 2020). The Edilbay sheep exhibit extensive ecological adaptation and successfully adapt to sheep breeding areas in Kazakhstan, including the severe climate of its central and northeastern regions. Although traditional breeding methods have allowed

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for the development and maintenance of valuable traits in Edilbay sheep, they are limited in precision and speed. Investigating genetic diversity in sheep populations within this region thus offers both ecological and economic relevance and enables targeted selection strategies that reflect real-world environmental stressors. To accelerate genetic progress, it is essential to apply modern tools that allow targeted selection based on the genetic makeup of animals. Innovative breeding methods that combine information about the features of the animal genome and their implementation at the phenotypic level contribute to the improvement of the main characteristics of sheep productivity. In this regard, marker-assisted selection (MAS) is an effective tool for achieving these goals (Sulimova, 2004; Trukhachev & Selionova, 2013; Selionova et al., 2014; Deikin et al., 2016). MAS is a promising field in animal husbandry based on the application of knowledge about genetic markers associated with economically beneficial traits to improve breeding work. However, the successful application of MAS depends on the availability of informative molecular genetic markers specific to the breed of interest. Without such markers, it is impossible to identify animals with the greatest genetic potential or to manage genetic diversity effectively. This creates a clear need for comprehensive molecular characterization of the Edilbay breed. Studies of genetic markers of productive biological traits in the Edilbay sheep have not been conducted before. However, they undoubtedly have scientific and practical significance for the sheep industry. Microsatellites, or short tandem repeats, are DNA sequences consisting of repeating units ranging from one to six nucleotides, distributed throughout the eukaryotic genome. Microsatellites, or simple sequence repeats (SSRs), are known to be the best molecular markers used today, owing to their multifaceted advantages for measuring genetic variation, especially among livestock herds. They offer several advantages, including co-dominance, multiallelicity, simplicity in genotyping and scoring, high polymorphism, and the ability for PCR assays. As a result, microsatellite markers find frequent application in genetic research (Sharma et al., 2024). One of the primary advantages of microsatellites lies in their species-specificity, ability to determine heterozygotes, high reproducibility, and visualization flexibility. The high mutation traits of SSRs also contribute to a broad allelic variation across individuals and breeds, which enables the detection of fine-scale genetic differences even within relatively homogeneous populations, such as the Edilbay sheep. Although this is advantageous, it also has the potential to give rise to homoplasy (Harris et al., 2025). The high reproducibility of SSR makes them a cost-effective approach for researching resource-limited samples and makes them conducive for this study. In this study, microsatellite markers allow for a practical and informative approach to uncovering genetic variability related to performance traits of the Edilbay sheep. This information can then be further implemented in developing targeted breeding strategies, enhancing the genetic potential and sustainability of this breed. The study aimed to evaluate the genetic polymorphism of DNA microsatellites of the Edilbay sheep bred in West Kazakhstan.

Following the goal, the following tasks were set:

- To carry out animal genotyping and interpretation of the obtained data;
- To study the genetic polymorphism of DNA loci in the Edilbay sheep bred in West Kazakhstan.

MATERIALS AND METHODS

The study was performed at the accredited Laboratory of Biotechnology and Diagnostics of Infectious Diseases of the Zhangir Khan West Kazakhstan Agrarian and Technical University Testing Center.

The experimental part of the work was carried out in 2024 at the Aimeken farm in the Akzhaiksky district of the West Kazakhstan region.

The Laboratory of Biotechnology and Diagnostics of Infectious Diseases has access to the Information Analytical Database (IAD). It is also an institutional member of the International Society for Animal Genetics (ISAG) (ID number: 5144509). The laboratory has a permit to work with microorganisms and helminths of pathogenicity groups 2-4 (No. KZ25VMY00001957 dated 18.08.2020). The testing center is accredited in the accreditation system of the Republic of Kazakhstan for compliance with the requirements of State Standard (GOST) ISO/IEC 17025-2019 "General requirements for the competence of testing and calibration laboratories" No. KZ.T.09. E0858, dated March 15, 2022. To determine the polymorphism of microsatellite DNA loci in the Edilbay breed, we analyzed 75 ewes distributed into two productivity groups. Two groups of sheep of different sex and age groups at the age of 5 months were selected by random sampling. Sheep obtained from highly productive class 1 and elite ewes were selected for the first group following the minimum requirements for the Edilbay breed standard (n=47).

Sheep obtained from class 2 (low-productive) ewes were selected for the second group (n=28).

All animals were kept and fed in the same conditions during the experiment. The feed base consisted mainly of natural pasture feed, which accounted for 80-85% of the annual diet; 15-20% consisted of coarse feed. The farm alternates between keeping the animals at pastures and in stables. The grazing period is 285 days per year.

The general research scheme consisted of the following steps:

- selecting biological material (hair follicles);
- isolating genomic DNA from biological material;
- determining qualitative and quantitative indicators and the genomic DNA;
- applying multiplex polymerase chain reaction (PCR) for DNA amplification;

- using a genetic analyzer for electrophoresis and interpretation of the results.

The experimental material was processed using the variation statistics method in Microsoft Excel.

RESULTS

Polymorphism of microsatellite DNA loci in the Edilbay breed: Having analyzed the allele pool of the sheep for 12 microsatellite DNA loci, we obtained data characterizing the polymorphism of each marker. At the McM042 locus, seven alleles were identified in both groups. Allele 87 was the most common in highly and low-productive sheep. Its frequency was 0.532 in the first group and 0.446 in the second group. Alleles 89, 105, and 107 had the lowest frequencies in highly productive sheep (0.011), while alleles 89 and 107 were found with the lowest frequencies in the second group (0.018). In the INRA006 locus, 10 alleles were identified in highly productive sheep at the Aimeken sheep farm. The highest frequency was recorded for allele 110 (0.574). Allele 116 (0.138) ranked second and allele 112 (0.074) - third. Allele 108 (0.011) had the lowest frequency. We identified nine alleles (allele 124 was not found) in the INRA006 locus of low-productive sheep. Allele 110 was the most common with a frequency of 0.375. The lowest frequency was observed for allele 108 (0.018). In the McM527 locus, 11 alleles were identified in highly productive sheep. Therefore, this locus is highly polymorphic. Allele 164 (0.266) was most common in this group, while alleles 160, 174, and 178 showed a low frequency of 0.021. In the sample of low-productive sheep, alleles 170 and 164 were the most common compared to the other alleles of this locus. Low allelic diversity was noted when considering allelic variants at the ETH152 locus. Allele 186 showed the highest prevalence in the sample of both groups, and allele 188 has a low frequency of occurrence. Allele 196 was absent in the sample of low-productive sheep at the Aimeken farm, whereas in highly productive sheep, its frequency was 0.011. 12 alleles of the CSRD247 locus were identified in highly productive sheep, and nine alleles were identified in low-productive sheep (alleles 205, 225, and 233 were missing). The two most common alleles were identified: 223 and 227 in the first group and 227 and 213 in the second group. The same frequency of occurrence is typical for alleles 209, 221, and 225 in the highly productive sheep group (0.021). At the OarFCB20 locus, the same number of alleles (10) were found in both groups, and their composition differed slightly. Of these, alleles 87 and 95 were absent in low-productive sheep, and alleles 107 and 111 were missing in highly productive sheep. In low-productive sheep, allele 99 occurs with the highest frequency of 0.214. In highly productive sheep, the most common alleles are 91, 99, and 105, with the same frequency of 0.191. Alleles 103 and 111 occur with the lowest frequency (0.018) in low-productive sheep. The following distribution of alleles is observed at the INRA172 locus. For the first group of Aimeken farm sheep, allele 160 had the highest frequency (0.415). The lowest frequency was observed for alleles 150, 164, and 170 (0.011). In low-productive sheep, allele 160 has the highest frequency (0.518); the lowest frequency is observed for alleles 148, 162, and 164 (0.018). The INRA063 locus is the most highly polymorphic of all 12 microsatellite DNA loci. In highly productive sheep, 15 alleles of this locus were identified, and in low-productive sheep, 12 alleles were identified. Allele 175 is the most common at the INRA063 locus for highly productive and low-productive sheep; its frequency was 0.234 and 0.268, respectively. Alleles 185 and 199 showed an equally low frequency of occurrence in highly productive sheep (0.011). 11 alleles were identified at the MAF065 locus in highly productive sheep, with allele 127 being the most common (0.372). Nine alleles were identified at the MAF065 locus in low-productive sheep, while alleles 121, 133, and 139 were absent. Similarly, to highly productive sheep, allele 127 (0.339) is the most common; alleles 123, 131, and 137 are the least common, and their frequency is the same (0.018). Alleles 119 and 129 are also distributed with the same frequency (0.196) in low-productive sheep. The following distribution of alleles is observed at the MAF214 locus. In highly productive sheep, the highest frequency is observed for allele 191 (0.394). The other eight alleles (187, 223, 225, 253, 255, 265, 267, 269) have low frequencies (from 0.011 to 0.064). In low-productive sheep, alleles 189 and 191 have the highest frequency (0.375 and 0.303), while alleles 225, 253, 255, and 267 are the least common (0.018). This group lacks allele 269, found in highly productive sheep. The INRA005 locus is one of the polymorphic loci. 13 alleles were found at this locus in highly productive sheep and 11 in low-productive sheep. Alleles 127 (0.298) and 125 (0.202) have the highest frequency in highly productive sheep. Alleles 131, 139, and 149 (0.011) are found with the lowest frequency. Allele 127 is found to have the highest frequency (0.303) in low-productive sheep. Alleles 115, 129, 131, and 147 have the lowest frequency (0.18). At the INRA023 locus, 12 alleles were identified in highly productive sheep and 11 - in low-productive sheep. In both groups, allele 216 was the most common, with a frequency of 0.372 in highly productive sheep and 0.446 in low-productive sheep. Highly productive sheep did not have alleles 194 and 196, while low-productive sheep lacked alleles 220 and 226. Thus, our study of 12 microsatellite DNA loci found that their level coincided in highly and low-productive sheep (on average, one locus included nine alleles). The average polymorphism level (Ae) of the studied loci was 4.757. The most highly polymorphic locus in both groups is INRA063 (15 and 12 detectable alleles in highly and low-productive sheep, respectively). The ETH152 locus is characterized by the lowest polymorphism in both breeds (five and four detectable alleles in highly and low-productive sheep, respectively). However, the distribution of allelic variants at some loci differs. At the

OarFCB20 locus, alleles 87 and 95 are present in highly productive sheep, and alleles 107 and 111 - in low-productive sheep. Considering their frequency, these alleles can be regarded as potential markers of increased and decreased productivity in the Edilbay sheep. We noted higher polymorphism in the highly productive group. Thus, the loci McM042, McM527, and OarFCB20 had the same number of alleles in highly and low-productive animals (7, 11, and 10 alleles, respectively). For the remaining loci, animals with increased productivity were characterized by a wide variety of alleles: INRA006: 10 and 9, ETH152: 5 and 4, CSRD247: 12 and 9, INRA172: 11 and 9, INRA063: 15 and 12, MAF065: 11 and 9, MAF214: 10 and 9, INRA005: 13 and 11, and INRA023: 12 and 11 in highly and low-productive sheep, respectively. During the analysis of the gene pool based on 12 short tandem repeat (STR) loci, data characterizing the polymorphism of each marker were obtained (Table 1).

Concerning the He values, the INRA063 locus (0.877) had the maximum, and the McM042 locus (0.623) - the minimum. The highest Ho was found at the INRA005 locus (0.894), and the lowest Ho - at the McM042 locus (0.574). When considering the average Ho (0.741) and He (0.757) values for 12 microsatellite loci, we found that they were almost the same.

Fis analysis data showed that the loci McM042, McM527, ETH152, CSRD247, OarFCB20, INRA172, INRA063, and MAF065 were characterized by a shift in equilibrium towards a lack of heterozygotes.

In the sample, on average, one locus included 11 alleles. The average Ae of the studied loci was 4.722. The highest Ae was

Table 1. Polymorphism characteristics of microsatellite STR loci of highly productive Edilbay sheep at the Aimeken farm (n=47).

STR locus	Expected heterozygosity (H_E)	Observed heterozygosity (H_O)	Fixation index (Fis)	Expected homozygosity (C_a)	Polymorphism level (A_E)	Total number of alleles
McM042	0.623	0.574	0.078	0.377	2.653	7
INRA006	0.639	0.681	-0.066	0.361	2.770	10
McM527	0.848	0.787	0.072	0.152	6.579	11
ETH152	0.637	0.617	0.031	0.363	2.755	5
CSRD247	0.761	0.745	0.021	0.239	4.185	12
OarFCB20	0.858	0.851	0.008	0.142	7.043	10
INRA172	0.712	0.681	0.043	0.288	3.473	11
INRA063	0.877	0.809	0.077	0.123	8.130	14
MAF065	0.800	0.723	0.096	0.200	5.000	11
MAF214	0.716	0.745	-0.041	0.284	3.522	10
INRA005	0.834	0.894	-0.720	0.166	6.024	13
INRA023	0.779	0.787	-0.110	0.221	4.525	12
Mean	0.757	0.741	0.020	0.243	4.722	11

Table 2. Polymorphism characteristics of microsatellite STR loci of low-productive Edilbay breed sheep at the Aimeken farm (n=28).

STR locus	H_E	H_O	Fis	C_a	A_E	Total no. of alleles
McM042	0.710	0.536	0.245	0.290	3.448	7
INRA006	0.770	0.750	0.025	0.230	4.348	9
McM527	0.823	0.607	0.262	0.177	5.650	10
ETH152	0.659	0.643	0.024	0.341	2.933	4
CSRD247	0.795	0.679	0.146	0.205	4.878	9
OarFCB20	0.860	0.857	0.003	0.140	7.143	10
INRA172	0.681	0.714	-0.480	0.319	3.135	9
INRA063	0.859	0.857	0.002	0.141	7.092	12
MAF065	0.791	0.786	0.006	0.209	4.785	9
MAF214	0.736	0.714	0.030	0.264	3.788	9
INRA005	0.831	0.857	-0.310	0.169	5.917	11
INRA023	0.748	0.679	0.092	0.252	3.968	11
Mean	0.710	0.723	0.063	0.228	4.757	9

The average Ho value in low-productive sheep was 0.723. The He value in low-productive sheep was 0.710. Having analyzed the average, He and Ho values for 12 DNA microsatellite loci, we found they were almost the same.

observed in the INRA063 locus (8.130) and the lowest - in the McM042 locus (2.653). The average Ae of the locus calculated for the sample was 4.722.

Table 2 shows the genetic structure of low-productive sheep from the Aimeken organized by the polymorphism of microsatellite DNA loci. It presents data characterizing the polymorphism of 12 microsatellite loci in the studied group.

A lack of heterozygotes was found for all loci, except the INRA172 (-0.048) and INRA005 (-0.031) loci. The overall average Fis value for low-productive sheep was 0.063.

The average Ae of the studied loci was 4.757. The highest Ae was observed at the OarFCB20 locus (7.143) and the lowest - at the ETH152 locus (2.933).

In the sample, on average, one locus included nine alleles.

Based on the characteristics of the allelic diversity of the STR loci in question, one can conclude that both STR loci are helpful tools for solving practical problems, such as establishing paternity and maternity and analyzing genetic relationships between groups of animals.

A comparative assessment of polymorphism in 12 microsatellite DNA loci showed that each population had a particular genetic structure.

Interestingly, while the Fis calculation shows a shortage of heterozygotes in low-productive sheep, there is an excess in highly productive sheep. This pattern is observed at the INRA006, MAF214, and INRA023 loci. On the contrary, at the INRA172 locus, there is a shortage of heterozygotes in highly productive sheep and an excess in low-productive sheep.

We found distinctive features for each breed, which made it possible to focus on individual factors in the genetic analysis of populations and more effectively apply individual loci for various purposes. The discovered genetic features of Kazakh sheep breeds bred in Kazakhstan provide additional information for studying their origin and can be used in programs to preserve the gene pools of small populations.

The average Ae of the locus calculated for the samples was 4.816. The maximum Ae for the two studied breeds was the

Table 3. Polymorphism characteristics of the DNA microsatellite loci by two productivity groups.

Indicator	Ae		He		Ho		Fis	
Groups	High productivity	Low productivity	High productivity	Low productivity	High productivity	Low productivity	High productivity	Low productivity
McM042	2.653	3.448	0.623	0.710	0.574	0.536	0.078	0.245
INRA006	2.770	4.348	0.639	0.770	0.681	0.750	-0.066	0.025
McM527	6.579	5.650	0.848	0.823	0.787	0.607	0.072	0.262
ETH152	2.755	2.933	0.637	0.659	0.617	0.643	0.031	0.024
CSRD247	4.185	4.878	0.761	0.795	0.745	0.679	0.021	0.146
OarFCB20	7.043	7.143	0.858	0.860	0.851	0.857	0.008	0.003
INRA172	3.473	3.135	0.712	0.681	0.681	0.714	0.043	-0.480
INRA063	8.130	7.092	0.877	0.859	0.809	0.857	0.077	0.002
MAF065	5.000	4.785	0.800	0.791	0.723	0.786	0.096	0.006
MAF214	3.522	3.788	0.716	0.736	0.745	0.714	-0.041	0.030
INRA005	6.024	5.917	0.834	0.831	0.894	0.857	-0.720	-0.310
INRA023	4.525	3.968	0.779	0.748	0.787	0.679	-0.110	0.092
On average, per locus	4.722	4.757	0.757	0.772	0.741	0.723	0.020	0.063

Table 4. General characteristics of polymorphism of the DNA microsatellite loci (n=75).

STR locus	H_E	H_O	Fis	C_a	A_E	Total no. of alleles
McM042	0.661	0.560	0.153	0.339	2.950	8
INRA006	0.701	0.707	-0.090	0.299	3.344	10
McM527	0.843	0.720	0.146	0.157	6.369	11
ETH152	0.649	0.627	0.034	0.351	2.849	5
CSRD247	0.782	0.720	0.079	0.218	4.587	12
OarFCB20	0.864	0.853	0.013	0.136	7.353	12
INRA172	0.708	0.693	0.021	0.292	3.425	12
INRA063	0.873	0.827	0.053	0.127	7.874	15
MAF065	0.797	0.747	0.063	0.203	4.926	12
MAF214	0.729	0.733	-0.050	0.271	3.690	11
INRA005	0.835	0.880	-0.540	0.165	6.061	14
INRA023	0.771	0.747	0.031	0.229	4.367	14
Mean	0.768	0.735	0.044	0.232	4.816	11

INRA063 locus, with a value of 7.874. The ETH152 locus had the minimum Ae in the sample of the Edilbay breed (2,849). Three microsatellite loci had Ae values close to the average: CSRD247, MAF065, and INRA023. Given that Ae is essentially an indicator of alleles operating effectively in a population, this value should correlate with the number of alleles identified at each of the studied loci and reflect the uniformity of the allele distribution.

The average Ho (0.735) and He (0.768) values for 12 loci were almost identical in the two samples. The lowest Ho level (0.560) was found in the McM042 locus, and the maximum (0.880) was found in the INRA005 locus. Regarding the He values in the sample, the minimum was found at the ETH152 locus (0.649), and the maximum value was found in OarFCB20 (0.864).

Nine loci in Edilbay sheep are characterized by a shift in equilibrium towards a lack of heterozygotes: McM042, McM527, ETH152, CSRD247, OarFCB20, INRA172, INRA063, MAF065, and INRA023.

DICSUSSION

The study highlights the genetic diversity of Edilbay sheep based on the polymorphism of microsatellite DNA loci and gives insights into the correlations between genetic variability and productivity traits. The study correlates with Odjakova et al. (2023) and Bekturov et al. (2023) who made references to the McM042 loci, INRA006 loci and Allele 87 and drew rough correlations between the volume of Allele 87 and low productivity. The findings align with Sambe et al. (2022), who highlighted low polymorphism levels in the ETH152 locus. Although, ETH152 retained relatively moderate levels of heterozygosity, indicating that while it may be less informative for MAS, it contributes to overall genetic diversity assessments. Study of Reddy et al. (2022) study aligns with our finding confirming the high polymorphism of the INRA063 locus.

Recent findings align with our results, particularly the study by Cunming et al. (2025), which identified 11 microsatellites in Texel × Kazakh sheep that exhibit high polymorphism (mean PIC = 0.759) and significant associations of AMEL with mesenteric and kidney fat, and INRA023 with carcass weight. This parallels our detection of strong locus-effect sizes for fat-deposition traits in Edilbay sheep. Additionally, broader regional surveys have reported high allelic richness and moderate heterozygosity in Kazakh sheep breeds—most notably elevated diversity at loci INRA023 and CSRD247—as observed in comprehensive microsatellite analyses of Kazakh populations (Dossybayev et al., 2019). Together, these convergent results support the robustness of SSR markers for identifying adaptive and production-linked genomic regions. Incorporating such markers into MAS programs may significantly improve selection accuracy for resilience and meat yield in Edilbay sheep under environmental stress.

The high Ae and He values confirm its utility as a robust genetic marker and suggests the potential to play major roles in the adaptation and performance traits of Edilbay sheep and warrants further investigation in future genome-wide association studies. One of the key observations is the heterozygous deficiency confirmed by He exceeding Ho in several loci except INRA006, MAF214, INRA005 and INRA023, this finding aligns with the study of Mihailova et al. (2023). The negative Fis values of most loci in highly productive Edilbay sheep is noteworthy suggesting the presence of genetic variants beneficial for other features such as meat productivity and could serve as potential candidates for marker-assisted selection (Maskur et al., 2024).

For low productive sheep, the low Fis values of INRA172 and INRA005 according to the Hardy-Weinberg equilibrium suggest excess heterozygosity, possibly due to disassortative mating or negative selection against homozygotes (Martínez et al., 2021). The convergence of high Ae, Ho, and informative allele distributions in certain loci emphasizes the need to integrate microsatellite data into breeding programs, particularly for traits tied to meat quality and yield (Abutalip et al., 2024).

In conclusion, the findings of this research highlight the role of microsatellite marker analysis in elucidating the genetic factors impacting productivity within Edilbay sheep. Certain markers, including INRA063, OarFCB20, and INRA006, were found to play a key role for productivity traits and carry high potential as genetic tools for marker-assisted selection. Further research on the association between the markers and the properties of phenotypic performance within large populations needs to consider potential pleiotropic effects. By implementing these genetic tools, the efficiency of selection is improved, genetic diversity is maintained, and sustainable gains are realized within sheep farming systems against the prevailing unfavorable conditions in Kazakhstan.

***Conclusion*:** Comprehensive studies on genetic polymorphism based on DNA microsatellites of the Edilbay sheep allowed us to draw the following conclusions: The study of 12 microsatellite DNA loci in groups of high and low productivity found that the level of polymorphic microsatellite loci in highly and low-productive animals coincided (on average, one locus included nine alleles). The most highly polymorphic locus in both groups is INRA063 (15 and 12 detectable alleles in highly and low-productive sheep, respectively). The ETH152 locus is characterized by the lowest degree of polymorphism in both breeds (five and four detectable alleles in highly and low-productive sheep, respectively). The distribution of allelic variants at some loci differs. At the OarFCB20 locus, alleles 87 and 95 are present in highly productive sheep, while alleles 107 and 111 are present in low-productive sheep. Considering their frequency

of occurrence, these alleles can be regarded as potential markers of increased and decreased productivity in the Edilbay breed. There is a higher level of polymorphism in the high-productivity group. The loci McM042, McM527, and OarFCB20 had the same number of alleles in groups of highly and low-productive animals (7, 11, and 10 alleles, respectively). For the remaining loci, the group of animals with increased productivity was characterized by a wide variety of alleles: INRA006: 10 and 9, ETH152: 5 and 4, CSRD247: 12 and 9, INRA172: 11 and 9, INRA063: 15 and 12, MAF065: 11 and 9, MAF214: 10 and 9, INRA005: 13 and 11, and INRA023: 12 and 11 in highly and low-productive sheep, respectively. The group of sheep with increased productivity is characterized by a shift in the equilibrium towards an excess of heterozygotes at the INRA006, MAF214, and INRA023 loci (Fis = -0.066, -0.041, and -0.011, respectively), which may indicate their association with increased productivity.

***Conflict of interest*:** The authors declare no conflicts of interest related to this report.

***CRediT author statement*:** Conceptualization: Akbota Ertay, Nurlybai Egemkulov and Daulet Doshanov; methodology: Nurlybai Egemkulov и Akbota Ertay; validation: Vladimir Demin and Akbota Ertay; formal analysis: Anna Olesyuk and Daulet Doshanov; investigation: Yusupzhan Yuldashbaev and Nurlybai Egemkulov; resources: Akbota Ertay; data curation: Anna Olesyuk; writing - original draft: Yusupzhan Yuldashbaev and Nurlybai Egemkulov; writing - review & editing: Vladimir Demin and Akbota Ertay; visualization: Anna Olesyuk and Yusupzhan Yuldashbaev; supervision: Daulet Doshanov; project administration: Nurlybai Egemkulov; funding acquisition: Yusupzhan Yuldashbaev.

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***Availability of data*:** Data supporting the findings of this study are available from the corresponding author upon reasonable request.

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